

MiniMUGA Background Analysis v0008

Sample ID	Shiota/GCGRSR CR.58																
Neogen ID	AAAA-6021																
Summary	The genotype of this sample is of excellent quality. It is male and close to inbred, and likely a mix of multiple C57BL/6 substrains and 129S6/SvEvTac.																
	Diagnostic SNPs indicate the presence of the background strain groups C57BL/6 and the substrains C57BL/6J. The sample contains the following genetic constructs: Bovine growth hormone poly A signal sequence, Cre recombinase, hCMV enhancer version a, hCMV enhancer version b, "Reddish" fluorescent protein (tdTomato, mCherry)																
Genotyping Quality	Excellent (2 N calls) All reported results are dependent on genotyping quality.																
Chromosomal Sex	XY																
Inbreeding Estimate	Close to Inbred (66 H calls at autosomal, X, and PAR chromosome markers)																
Inbreeding and Genotyping Quality (Plot)																	
Constructs Detected	BlastR	bpA	Cas9	chlor	Cre	DTA	g_FP	hCMV_a	hCMV_b	hTK_pr	iCre	IRES	Luc	r_FP	rtTA	SV40	tTA
	-	+	-	-	+	-	-	+	+	-	-	-	-	+	-	-	-
Primary Background (Autosomes, X Chromosome)	Strain		Total	Consistent	Inconsistent	Heterozygous		Excluded									
	multiple C57BL/6 substrains		9721	9245 (99.4%)	1 (0.0%)	56 (0.6%)		419									
Secondary Background (Autosomes, X Chromosome)	Strain		Total	Explained		Unexplained		Excluded									
	129S6/SvEvTac		57	55 (0.6%)		2 (0.0%)		0 (0.0%)									
			55 Clustered	55 Clustered		0 Clustered											
Background Ideogram																	
Backgrounds Detected (Diagnostic Alleles)	Diagnostic Alleles Observed																
	Substrain		Homozygous	Heterozygous	Potential	% Observed											
	C57BL/6J		144	7	156	96.8%											
	Strain Group		Homozygous	Heterozygous	Potential	% Observed											
C57BL/6		5	1	21	28.6%												
(B6N-Tyr/BrdCrCrI, C57BL/6J, C57BL/6JBomTac,																	

